

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/964,858B
Source: IFW/6
Date Processed by STIC: 6/9/06

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,858B

DATE: 06/09/2006
TIME: 09:49:21

Input Set : A:\Sequence_09-964,858.txt
Output Set: N:\CRF4\06092006\I964858B.raw

3 <110> APPLICANT: HOSTETTER, Margaret K.
4 DEVORE-CARTER, Denise
6 <120> TITLE OF INVENTION: ANTIBODIES TO THE PROPEPTIDE OF CANDIDA ALBICANS
8 <130> FILE REFERENCE: P07274US02/BAS
10 <140> CURRENT APPLICATION NUMBER: US 09/964,858B
11 <141> CURRENT FILING DATE: 2001-09-28
13 <150> PRIOR APPLICATION NUMBER: US 60/237,082
14 <151> PRIOR FILING DATE: 2000-09-28
16 <160> NUMBER OF SEQ ID NOS: 13
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1664
22 <212> TYPE: PRT
23 <213> ORGANISM: Candida albicans
25 <400> SEQUENCE: 1
27 Met Asn Ser Thr Pro Ser Lys Leu Leu Pro Ile Asp Lys His Ser His
28 1 5 10 15
31 Leu Gln Leu Gln Pro Gln Ser Ser Ser Ala Ser Ile Phe Asn Ser Pro
32 20 25 30
35 Thr Lys Pro Leu Asn Phe Pro Arg Thr Asn Ser Lys Pro Ser Leu Asp
36 35 40 45
39 Pro Asn Ser Ser Ser Asp Thr Tyr Thr Ser Glu Gln Asp Gln Glu Lys
40 50 55 60
43 Gly Lys Glu Glu Lys Lys Asp Thr Ala Phe Gln Thr Ser Phe Asp Arg
44 65 70 75 80
47 Asn Phe Asp Leu Asp Asn Ser Ile Asp Ile Gln Gln Thr Ile Gln His
48 85 90 95
51 Gln Gln Gln Pro Gln Gln Gln Gln Gln Leu Ser Gln Thr Asp Asn
52 100 105 110
55 Asn Leu Ile Asp Glu Phe Ser Phe Gln Thr Pro Met Thr Ser Thr Leu
56 115 120 125
59 Asp Leu Thr Lys Gln Asn Pro Thr Val Asp Lys Val Asn Glu Asn His
60 130 135 140
63 Ala Pro Thr Tyr Ile Asn Thr Ser Pro Asn Lys Ser Ile Met Lys Lys
64 145 150 155 160
67 Ala Thr Pro Lys Ala Ser Pro Lys Lys Val Ala Phe Thr Val Thr Asn
68 165 170 175
71 Pro Glu Ile His His Tyr Pro Asp Asn Arg Val Glu Glu Glu Asp Gln
72 180 185 190
75 Ser Gln Gln Lys Glu Asp Ser Val Glu Pro Pro Leu Ile Gln His Gln
76 195 200 205
79 Trp Lys Asp Pro Ser Gln Phe Asn Tyr Ser Asp Glu Asp Thr Asn Ala
80 210 215 220

Pb

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83 Ser Val Pro Pro Thr Pro Pro Leu His Thr Thr Lys Pro Thr Phe Ala
 84 225 230 235 240
 87 Gln Leu Leu Asn Lys Asn Asn Glu Val Asn Ser Glu Pro Glu Ala Leu
 88 245 250 255
 91 Thr Asp Met Lys Leu Lys Arg Glu Asn Phe Ser Asn Leu Ser Leu Asp
 92 260 265 270
 95 Glu Lys Val Asn Leu Tyr Leu Ser Pro Thr Asn Asn Asn Ser Lys
 96 275 280 285
 99 Asn Val Ser Asp Met Asp Ser His Leu Gln Asn Leu Gln Asp Ala Ser
 100 290 295 300
 103 Lys Asn Lys Thr Asn Glu Asn Ile His Asn Leu Ser Phe Ala Leu Lys
 104 305 310 315 320
 107 Ala Pro Lys Asn Asp Ile Glu Asn Pro Leu Asn Ser Leu Thr Asn Ala
 108 325 330 335
 111 Asp Ile Ser Leu Arg Ser Ser Gly Ser Ser Gln Ser Ser Leu Gln Ser
 112 340 345 350
 115 Leu Arg Asn Asp Asn Arg Val Leu Glu Ser Val Pro Gly Ser Pro Lys
 116 355 360 365
 119 Lys Val Asn Pro Gly Leu Ser Leu Asn Asp Gly Ile Lys Gly Phe Ser
 120 370 375 380
 123 Asp Glu Val Val Glu Ser Leu Leu Pro Arg Asp Leu Ser Arg Asp Lys
 124 385 390 395 400
 127 Leu Glu Thr Thr Lys Glu His Asp Ala Pro Glu His Asn Asn Glu Asn
 128 405 410 415
 131 Phe Ile Asp Ala Lys Ser Thr Asn Thr Asn Lys Gly Gln Leu Leu Val
 132 420 425 430
 135 Ser Ser Asp Asp His Leu Asp Ser Phe Asp Arg Ser Tyr Asn His Thr
 136 435 440 445
 139 Glu Gln Ser Ile Leu Asn Leu Leu Asn Ser Ala Ser Gln Ser Gln Ile
 140 450 455 460
 143 Ser Leu Asn Ala Leu Glu Lys Gln Arg Gln Thr Gln Glu Gln Glu Gln
 144 465 470 475 480
 147 Thr Gln Ala Ala Glu Pro Glu Glu Glu Thr Ser Phe Ser Asp Asn Ile
 148 485 490 495
 151 Lys Val Lys Gln Glu Pro Lys Ser Asn Leu Glu Phe Val Lys Val Thr
 152 500 505 510
 155 Ile Lys Lys Glu Pro Val Ser Ala Thr Glu Ile Lys Ala Pro Lys Arg
 156 515 520 525
 159 Glu Phe Ser Ser Arg Ile Leu Arg Ile Lys Asn Glu Asp Glu Ile Ala
 160 530 535 540
 163 Glu Pro Ala Asp Ile His Pro Lys Lys Glu Asn Glu Ala Asn Ser His
 164 545 550 555 560
 167 Val Glu Asp Thr Asp Ala Leu Leu Lys Lys Ala Leu Asn Asp Asp Glu
 168 565 570 575
 171 Glu Ser Asp Thr Thr Gln Asn Ser Thr Lys Met Ser Ile Arg Phe His
 172 580 585 590
 175 Ile Asp Ser Asp Trp Lys Leu Glu Asp Ser Asn Asp Gly Asp Arg Glu
 176 595 600 605
 179 Asp Asn Asp Asp Ile Ser Arg Phe Glu Lys Ser Asp Ile Leu Asn Asp

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180	610	615	620													
183	Val	Ser	Gln	Thr	Ser	Asp	Ile	Ile	Gly	Asp	Lys	Tyr	Gly	Asn	Ser	Ser
184	625															640
187	Ser	Glu	Ile	Thr	Thr	Lys	Thr	Leu	Ala	Pro	Pro	Arg	Ser	Asp	Asn	Asn
188																655
191	Asp	Lys	Glu	Asn	Ser	Lys	Ser	Leu	Glu	Asp	Pro	Ala	Asn	Asn	Glu	Ser
192																670
195	Leu	Gln	Gln	Gln	Leu	Glu	Val	Pro	His	Thr	Lys	Glu	Asp	Asp	Ser	Ile
196																685
199	Leu	Ala	Asn	Ser	Ser	Asn	Ile	Ala	Pro	Pro	Glu	Glu	Leu	Thr	Leu	Pro
200																700
203	Val	Val	Glu	Ala	Asn	Asp	Tyr	Ser	Ser	Phe	Asn	Asp	Val	Thr	Lys	Thr
204	705															720
207	Phe	Asp	Ala	Tyr	Ser	Ser	Phe	Glu	Glu	Ser	Leu	Ser	Arg	Glu	His	Glu
208																735
211	Thr	Asp	Ser	Lys	Pro	Ile	Asn	Phe	Ile	Ser	Ile	Trp	His	Lys	Gln	Glu
212																750
215	Lys	Gln	Lys	His	Gln	Ile	His	Lys	Val	Pro	Thr	Lys	Gln	Ile	Ile	
216																765
219	Ala	Ser	Tyr	Gln	Gln	Tyr	Lys	Asn	Glu	Gln	Glu	Ser	Arg	Val	Thr	Ser
220																780
223	Asp	Lys	Val	Lys	Ile	Pro	Asn	Ala	Ile	Gln	Phe	Lys	Lys	Phe	Lys	Glu
224	785															800
227	Val	Asn	Val	Met	Ser	Arg	Arg	Val	Val	Ser	Pro	Asp	Met	Asp	Asp	Leu
228																815
231	Asn	Val	Ser	Gln	Phe	Leu	Pro	Glu	Leu	Ser	Glu	Asp	Ser	Gly	Phe	Lys
232																830
235	Asp	Leu	Asn	Phe	Ala	Asn	Tyr	Ser	Asn	Asn	Thr	Asn	Arg	Pro	Arg	Ser
236																845
239	Phe	Thr	Pro	Leu	Ser	Thr	Lys	Asn	Val	Leu	Ser	Asn	Ile	Asp	Asn	Asp
240																860
243	Pro	Asn	Val	Val	Glu	Pro	Pro	Glu	Pro	Lys	Ser	Tyr	Ala	Glu	Ile	Arg
244	865															880
247	Asn	Ala	Arg	Arg	Leu	Ser	Ala	Asn	Lys	Ala	Ala	Pro	Asn	Gln	Ala	Pro
248																895
251	Pro	Leu	Pro	Pro	Gln	Arg	Gln	Pro	Ser	Ser	Thr	Arg	Ser	Asn	Ser	Asn
252																910
255	Lys	Arg	Val	Ser	Arg	Phe	Arg	Val	Pro	Thr	Phe	Glu	Ile	Arg	Arg	Thr
256																925
259	Ser	Ser	Ala	Leu	Ala	Pro	Cys	Asp	Met	Tyr	Asn	Asp	Ile	Phe	Asp	Asp
260																940
263	Phe	Gly	Ala	Gly	Ser	Lys	Pro	Thr	Ile	Lys	Ala	Glu	Gly	Met	Lys	Thr
264	945															960
267	Leu	Pro	Ser	Met	Asp	Lys	Asp	Asp	Val	Lys	Arg	Ile	Leu	Asn	Ala	Lys
268																975
271	Lys	Gly	Val	Thr	Gln	Asp	Glu	Tyr	Ile	Asn	Ala	Lys	Leu	Val	Asp	Gln
272																990
275	Lys	Pro	Lys	Lys	Asn	Ser	Ile	Val	Thr	Asp	Pro	Glu	Asp	Arg	Tyr	Glu
276																1005
	995					1000										

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279 Glu Leu Gln Gln Thr Ala Ser Ile His Asn Ala Thr Ile Asp Ser
 280 1010 1015 1020
 283 Ser Ile Tyr Gly Arg Pro Asp Ser Ile Ser Thr Asp Met Leu Pro
 284 1025 1030 1035
 287 Tyr Leu Ser Asp Glu Leu Lys Lys Pro Pro Thr Ala Leu Leu Ser
 288 1040 1045 1050
 291 Ala Asp Arg Leu Phe Met Glu Gln Glu Val His Pro Leu Arg Ser
 292 1055 1060 1065
 295 Asn Ser Val Leu Val His Pro Gly Ala Gly Ala Ala Thr Asn Ser
 296 1070 1075 1080
 299 Ser Met Leu Pro Glu Pro Asp Phe Glu Leu Ile Asn Ser Pro Ala
 300 1085 1090 1095
 303 Arg Asn Val Ser Asn Asn Ser Asp Asn Val Ala Ile Ser Gly Asn
 304 1100 1105 1110
 307 Ala Ser Thr Ile Ser Phe Asn Gln Leu Asp Met Asn Phe Asp Asp
 308 1115 1120 1125
 311 Gln Ala Thr Ile Gly Gln Lys Ile Gln Glu Gln Pro Ala Ser Lys
 312 1130 1135 1140
 315 Ser Ala Asn Thr Val Arg Gly Asp Asp Asp Gly Leu Ala Ser Ala
 316 1145 1150 1155
 319 Pro Glu Thr Pro Arg Thr Pro Thr Lys Lys Glu Ser Ile Ser Ser
 320 1160 1165 1170
 323 Lys Pro Ala Lys Leu Ser Ser Ala Ser Pro Arg Lys Ser Pro Ile
 324 1175 1180 1185
 327 Lys Ile Gly Ser Pro Val Arg Val Ile Lys Lys Asn Gly Ser Ile
 328 1190 1195 1200
 331 Ala Gly Ile Glu Pro Ile Pro Lys Ala Thr His Lys Pro Lys Lys
 332 1205 1210 1215
 335 Ser Phe Gln Gly Asn Glu Ile Ser Asn His Lys Val Arg Asp Gly
 336 1220 1225 1230
 339 Gly Ile Ser Pro Ser Ser Gly Ser Glu His Gln Gln His Asn Pro
 340 1235 1240 1245
 343 Ser Met Val Ser Val Pro Ser Gln Tyr Thr Asp Ala Thr Ser Thr
 344 1250 1255 1260
 347 Val Pro Asp Glu Asn Lys Asp Val Gln His Lys Pro Arg Glu Lys
 348 1265 1270 1275
 351 Gln Lys Gln Lys His His His Arg His His His His His His Lys
 352 1280 1285 1290
 355 Gln Lys Thr Asp Ile Pro Gly Val Val Asp Asp Glu Ile Pro Asp
 356 1295 1300 1305
 359 Val Gly Leu Gln Glu Arg Gly Lys Leu Phe Phe Arg Val Leu Gly
 360 1310 1315 1320
 363 Ile Lys Asn Ile Asn Leu Pro Asp Ile Asn Thr His Lys Gly Arg
 364 1325 1330 1335
 367 Phe Thr Leu Thr Leu Asp Asn Gly Val His Cys Val Thr Thr Pro
 368 1340 1345 1350
 371 Glu Tyr Asn Met Asp Asp His Asn Val Ala Ile Gly Lys Glu Phe
 372 1355 1360 1365
 375 Glu Leu Thr Val Ala Asp Ser Leu Glu Phe Ile Leu Thr Leu Lys

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376	1370	1375	1380												
379	Ala	Ser	Tyr	Glu	Lys	Pro	Arg	Gly	Thr	Leu	Val	Glu	Val	Thr	Glu
380	1385		1390		1395										
383	Lys	Lys	Val	Val	Lys	Ser	Arg	Asn	Arg	Leu	Ser	Arg	Leu	Phe	Gly
384	1400		1405		1410										
387	Ser	Lys	Asp	Ile	Ile	Thr	Thr	Thr	Lys	Phe	Val	Pro	Thr	Glu	Val
388	1415		1420		1425										
391	Lys	Asp	Thr	Trp	Ala	Asn	Lys	Phe	Ala	Pro	Asp	Gly	Ser	Phe	Ala
392	1430		1435		1440										
395	Arg	Cys	Tyr	Ile	Asp	Leu	Gln	Gln	Phe	Glu	Asp	Gln	Ile	Thr	Gly
396	1445		1450		1455										
399	Lys	Ala	Ser	Gln	Phe	Asp	Leu	Asn	Cys	Phe	Asn	Glu	Trp	Glu	Thr
400	1460		1465		1470										
403	Met	Ser	Asn	Gly	Asn	Gln	Pro	Met	Lys	Arg	Gly	Lys	Pro	Tyr	Lys
404	1475		1480		1485										
407	Ile	Ala	Gln	Leu	Glu	Val	Lys	Met	Leu	Tyr	Val	Pro	Arg	Ser	Asp
408	1490		1495		1500										
411	Pro	Arg	Glu	Ile	Leu	Pro	Thr	Ser	Ile	Arg	Ser	Ala	Tyr	Glu	Ser
412	1505		1510		1515										
415	Ile	Asn	Glu	Leu	Asn	Asn	Glu	Gln	Asn	Asn	Tyr	Phe	Glu	Gly	Tyr
416	1520		1525		1530										
419	Leu	His	Gln	Glu	Gly	Gly	Asp	Cys	Pro	Ile	Phe	Lys	Lys	Arg	Phe
420	1535		1540		1545										
423	Phe	Lys	Leu	Met	Gly	Thr	Ser	Leu	Leu	Ala	His	Ser	Glu	Ile	Ser
424	1550		1555		1560										
427	His	Lys	Thr	Arg	Ala	Lys	Ile	Asn	Leu	Ser	Lys	Val	Val	Asp	Leu
428	1565		1570		1575										
431	Ile	Tyr	Val	Asp	Lys	Glu	Asn	Ile	Asp	Arg	Ser	Asn	His	Arg	Asn
432	1580		1585		1590										
435	Phe	Ser	Asp	Val	Leu	Leu	Leu	Asp	His	Ala	Phe	Lys	Ile	Lys	Phe
436	1595		1600		1605										
439	Ala	Asn	Gly	Glu	Leu	Ile	Asp	Phe	Cys	Ala	Pro	Asn	Lys	His	Glu
440	1610		1615		1620										
443	Met	Lys	Ile	Trp	Ile	Gln	Asn	Leu	Gln	Glu	Ile	Ile	Tyr	Arg	Asn
444	1625		1630		1635										
447	Arg	Phe	Arg	Arg	Gln	Pro	Trp	Val	Asn	Leu	Met	Leu	Gln	Gln	Gln
448	1640		1645		1650										
451	Gln	Gln	Gln	Gln	Gln	Gln	Ser	Ser	Gln	Gln					
452	1655		1660												
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456	<211>	LENGTH:	5194												
457	<212>	TYPE:	DNA												
458	<213>	ORGANISM:	Candida	albicans											
460	<400>	SEQUENCE:	2												
461	ccccaaaaaag	ataaaataaa	aacaaaacaa	aacaaaagta	ctaacaattt	attgaaactt									60
463	ttaattttta	ataaaagaatc	agtagatcta	ttgttaaaag	aatatgaactc	aactccaagt									120
465	aaatttattac	cgatagataa	acattctcat	ttacaattac	agcctcaatc	gtcctcggca									180
467	tcaatattta	attccccaaac	aaaaccattg	aatttccccaa	gaacaaattc	caagccgagt									240
469	ttagatccaa	attcaagctc	tgatacctac	actagcgaac	aagatcaaga	gaaagggaaa									300

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/09/2006
PATENT APPLICATION: US/09/964,858B TIME: 09:49:22

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 3

VERIFICATION SUMMARY

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Input Set : A:\Sequence_09-964,858.txt

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L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0